



SEQUENCE LISTING

<110> THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
HUMAN SERVICES  
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Hayes, Mark P.  
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<140> US 10/615,723  
<141> 2003-07-08  
<150> US 09/744,754  
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 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
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 aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
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 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
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 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80  
 ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288  
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95  
 gaa gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110  
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
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Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
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Ser Leu Arg Ser Lys Glu  
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20          25          30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc      144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35          40          45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc      192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50          55          60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc      240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65          70          75          80

ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc      288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85          90          95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg      336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100          105          110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act      384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115          120          125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gaa gtt gtc      432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130          135          140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa      480
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

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Ser Leu Arg Ser Lys Glu  
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Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser	Leu	Phe	Ser	Cys	Leu	Lys	Asp	
		20					25					30				

aga	cgt	gac	ttt	gga	ttt	ccc	cag	gag	gag	ttt	ggc	aac	cag	ttc	caa	144
Arg	Arg	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Gly	Asn	Gln	Phe	Gln	
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aag	gct	gaa	acc	atc	cct	gtc	ctc	cat	gag	atg	atc	cag	cag	atc	ttc	192
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Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
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Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
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Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
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Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
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Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn  
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Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu  
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Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
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Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
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85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
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100 105 110

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Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
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Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
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Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
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Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
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Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
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Ser Leu Arg Ser Lys Glu

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 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

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cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
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 50 55 60

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ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc 288  
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 85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
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 130 135 140

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 Ser Leu Arg Ser Lys Glu  
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
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Ser Leu Arg Ser Lys Glu  
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 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80  
 ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288  
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95  
 gaa gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met  
 100 105 110  
 aat gtg gac tcc atc ttg gct gtg aag aaa tac ttc caa aga atc act 384  
 Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
 ctt tat ctg aca gag aag aaa tac agc cct tgt gct tgg gag gtt gtc 432  
 Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
 aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu  
 145 150 155 160  
 aga tta agg agg aag gaa tg 500



Arg Leu Arg Arg Lys Glu  
165

<210> 34  
<211> 166  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Gene Fusion

<400> 34

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met  
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr  
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu  
145 150 155 160

Arg Leu Arg Arg Lys Glu  
165

<210> 35  
 <211> 500  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<220>  
 <221> CDS  
 <222> (1) .. (498)

<400> 35  
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48  
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80

ctc cta gaa aaa ttt tac act gaa ctt aac cag cag ctg aat gac ctc 288  
 Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu

<210> 36  
 <211> 166  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<400> 36

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

Ser Leu Arg Ser Lys Glu  
 165

<210> 37  
 <211> 500  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<220>  
 <221> CDS  
 <222> (1)..(498)

<400> 37  
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48  
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15  
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30  
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80  
 ctc cta gaa aaa ttt tcc act gaa ctt tac cag cag ctg aat gac ctc 288  
 Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95  
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110  
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160  
 agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu  
 165

<210> 38  
 <211> 166  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<400> 38

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr  
 65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

Ser Leu Arg Ser Lys Glu  
 165

<210> 39

<211> 500  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<220>  
 <221> CDS  
 <222> (1)..(498)

<400> 39  
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48  
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80

ctc cta gac aaa ttc tcc act gaa ctc tac cag cag ctg aat gac ctc 288  
 Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95

gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu  
 165

<210> 40  
 <211> 166  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<400> 40

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80

Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

Ser Leu Arg Ser Lys Glu  
 165

<210> 41  
 <211> 500

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<220>  
 <221> CDS  
 <222> (1)..(498)

<400> 41  
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48  
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15  
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96  
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30  
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45  
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192  
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60  
 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240  
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80  
 ctc cta gac aaa ttc tac act gaa ctc aac cag cag ctg aat gac ctc 288  
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95  
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336  
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110  
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384  
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125  
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432  
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140  
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480  
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160  
 agt tta aga agt aag gaa tg 500  
 Ser Leu Arg Ser Lys Glu  
 165



<210> 42  
 <211> 166  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Gene Fusion

<400> 42

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile  
 1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp  
 20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe  
 35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr  
 50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser  
 65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu  
 85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met  
 100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr  
 115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val  
 130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu  
 145 150 155 160

Ser Leu Arg Ser Lys Glu  
 165

<210> 43  
 <211> 14  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> misc\_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc\_feature

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid

<400> 43

Leu Asp Lys Phe Xaa Thr Glu Leu Xaa Gln Gln Leu Asn Asp  
1 5 10

<210> 44

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide

<220>

<221> misc\_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc\_feature

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid

<400> 44

Leu Glu Lys Phe Xaa Thr Glu Leu Xaa Gln Gln Leu Asn Asp  
1 5 10